

SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Methods for enhancing exogenous epitope display on MHC class
through inhibition of TAP activity

<130> D3-A0102P

<140>

<141>

<150> JP 2002-288394

<151> 2002-10-01

<160> 54

<170> PatentIn Ver. 2.0

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<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 1

Gly Gly Gly Ser

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<211> 5

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Gly Gly Gly Gly Ser

1

5

<210> 3

<211> 10

<212> PRT

<213> Artificial Sequence

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synthesized sequence

<400> 3

Gly	Gly	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly
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<212> PRT

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synthesized sequence

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Ser	Gly	Gly	Gly
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<210> 5

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synthesized sequence

<400> 5

Gly Gly Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 1 5 10 15

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 20 25 30

<210> 6

<211> 10

<212> PRT

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<400> 6

Gly Gly Ser Gly Gly Gly Ala Ser Gly Gly
 1 5 10

<210> 7

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<400> 7

gggcgggatcc ggactcagaa tctccccaga cgccgag

37

<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially
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ccgcctcgag ctggggagga aacaggtcag catgggaac

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<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially synthesized sequence

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<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 10

aatttggaat tcatccaatc caaatgcggc

30

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<212> PRT

<213> Artificial Sequence

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<400> 11

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially
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<212> DNA

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<223> Description of Artificial Sequence: artificially
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tcc

63

<210> 14

<211> 63

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially
synthesized sequence

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tcc

63

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<212> DNA

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<223> Description of Artificial Sequence: artificially synthesized sequence

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<212> DNA

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<211> 80

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (21).. (80)

<400> 18

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Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala

1 5 10

cta ctc tct ctt tct ggc ctg gag gct

80

Leu Leu Ser Leu Ser Gly Leu Glu Ala

15 20

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<400> 19

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser

1 5 10 15

Gly Leu Glu Ala

20

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

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<220>

<221> CDS

<222> (1).. (30)

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 1 5 10

30

<210> 21

<211> 10

<212> PRT

<213> Artificial Sequence

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Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe
 1 5 10

<210> 22

<211> 33

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 synthesized sequence

<220>

<221> CDS

<222> (1).. (33)

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 1 5 10

33

<210> 23

<211> 11

<212> PRT

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<400> 23

Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile

1 5 10

<210> 24

<211> 60

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1).. (60)

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1 5 10 15	

act cca aag att	60
Thr Pro Lys Ile	
20	

<210> 25

<211> 20

<212> PRT

<213> Artificial Sequence

<400> 25

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1 5 10 15	

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20	

<210> 26

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<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1).. (18)

<400> 26

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Lys Trp Asp Arg Asp Met
1 5

gtgaaagttc atcgcgccgc c 69

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 27

Lys Trp Asp Arg Asp Met
1 5

<210> 28

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 28

tgcggccgcc gtacgccgag gatggccgtc atggcgcccc g 41

<210> 29

<211> 71

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 29

ttgcggccgc gatgaacttt caccctaagt ttttcttact acggcgtacg tcacacttta 60

caagctgtga g

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<210> 30

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<221> CDS

<222> (21).. (38)

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gcggccgccg tacgccgagg atg gcc gtc atg gcg ccc

38

Met Ala Val Met Ala Pro

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<210> 31

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<400> 31

Met Ala Val Met Ala Pro

1

5

<210> 32

<211> 69

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<220>

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<222> (1).. (18)

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Leu Thr Ala Cys Lys Val

1

5

gtgaaagttc atcgcggccg c

69

<210> 33

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Leu Thr Ala Cys Lys Val

1

5

<210> 34

<211> 64

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially
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<400> 34

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aaat

64

<210> 35

<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially synthesized sequence

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<210> 36

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 36

tgcggccgcc actccttcac tatggatctc ttg 33

<210> 37

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

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<210> 38

<211> 53

<212> DNA

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<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

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<210> 39
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 <212> DNA
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<220>
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 <222> (43).. (60)

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 Met Ser Trp Ala
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ctg gaa 60
 Leu Glu
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<210> 40
 <211> 6
 <212> PRT
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<400> 40
 Met Ser Trp Ala Leu Glu
 1 5

<210> 41
 <211> 55
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<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (1).. (42)

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1 5 10	

tgatagcggc cgc	55
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<210> 42

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<212> PRT

<213> Artificial Sequence

<400> 42

Arg Asn Pro Val Thr Arg Gly Ala His His His His His His	
1 5 10	

<210> 43

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (41).. (58)

<400> 43

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Met Asp Leu Leu Ile	
1 5	

cgt	58
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Arg

<210> 44

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 44

Met Asp Leu Leu Ile Arg
 1 5

<210> 45

<211> 55

<212> DNA

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<223> Description of Artificial Sequence: artificially
 synthesized sequence

<220>

<221> CDS

<222> (1).. (42)

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 Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His
 1 5 10

tgatagcggc cgc 55

<210> 46

<211> 14

<212> PRT

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Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His
 1 5 10

<210> 47
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 <212> DNA
 <213> Homo sapiens

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 <222> (165).. (2588)
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 tatctagtga gcaggcggcc gctttcgatt tcgctttccc ctaa atg gct gag ctt 176
 Met Ala Glu Leu
 1
 ctc gcc agc gca gga tca gcc tgt tcc tgg gac ttt ccg aga gcc ccg 224
 Leu Ala Ser Ala Gly Ser Ala Cys Ser Trp Asp Phe Pro Arg Ala Pro
 5 10 15 20
 ccc tcg ttc cct ccc cca gcc gcc agt agg gga gga ctc ggc ggt acc 272
 Pro Ser Phe Pro Pro Pro Ala Ala Ser Arg Gly Gly Leu Gly Gly Thr
 25 30 35
 cgg agc ttc agg ccc cac cgg ggc gcg gag agt ccc agg ccc ggc cgg 320
 Arg Ser Phe Arg Pro His Arg Gly Ala Glu Ser Pro Arg Pro Gly Arg
 40 45 50
 gac cgg gac ggc gtc cga gtg cca atg gct agc tct agg tgt ccc gct 368
 Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser Arg Cys Pro Ala
 55 60 65
 ccc cgc ggg tgc cgc tgc ctc ccc gga gct tct ctc gca tgg ctg ggg 416
 Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu Ala Trp Leu Gly
 70 75 80
 aca gta ctg cta ctt ctc gcc gac tgg gtg ctg ctc cgg acc gcg ctg 464
 Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu Arg Thr Ala Leu
 85 90 95 100
 ccc cgc ata ttc tcc ctg ctg gtg ccc acc gcg ctg cca ctg ctc cgg 512

Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu Pro Leu Leu Arg	
105 110 115	
gtc tgg gcg gtg ggc ctg agc cgc tgg gcc gtg ctc tgg ctg ggg gcc	560
Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu Trp Leu Gly Ala	
120 125 130	
tgc ggg gtc ctc agg gca acg gtt ggc tcc aag agc gaa aac gca ggt	608
Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser Glu Asn Ala Gly	
135 140 145	
gcc cag ggc tgg ctg gct gct ttg aag cca tta gct gcg gca ctg ggc	656
Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala Ala Ala Leu Gly	
150 155 160	
ttg gcc ctg ccg gga ctt gcc ttg ttc cga gag ctg atc tca tgg gga	704
Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu Ile Ser Trp Gly	
165 170 175 180	
gcc ccc ggg tcc gcg gat agc acc agg cta ctg cac tgg gga agt cac	752
Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His Trp Gly Ser His	
185 190 195	
cct acc gcc ttc gtt gtc agt tat gca gcg gca ctg ccc gca gca gcc	800
Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu Pro Ala Ala Ala	
200 205 210	
ctg tgg cac aaa ctc ggg agc ctc tgg gtg ccc ggc ggt cag ggc ggc	848
Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly Gly Gln Gly Gly	
215 220 225	
tct gga aac cct gtg cgt cgg ctt cta ggc tgc ctg ggc tcg gag acg	896
Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu Gly Ser Glu Thr	
230 235 240	
cgc cgc ctc tcg ctg ttc ctg gtc ctg gtg gtc ctc tcc tct ctt ggg	944
Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu Ser Ser Leu Gly	
245 250 255 260	
gag atg gcc att cca ttc ttt acg ggc cgc ctc act gac tgg att cta	992
Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr Asp Trp Ile Leu	
265 270 275	
caa gat ggc tca gcc gat acc ttc act cga aac tta act ctc atg tcc	1040

Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu Thr Leu Met Ser	
280 285 290	
att ctc acc ata gcc agt gca gtg ctg gag ttc gtg ggt gac ggg atc	1088
Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val Gly Asp Gly Ile	
295 300 305	
tat aac aac acc atg ggc cac gtg cac agc cac ttg cag gga gag gtg	1136
Tyr Asn Asn Thr Met Gly His Val His Ser His Leu Gln Gly Glu Val	
310 315 320	
ttt ggg gct gtc ctg cgc cag gag acg gag ttt ttc caa cag aac cag	1184
Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe Gln Gln Asn Gln	
325 330 335 340	
aca ggt aac atc atg tct cgg gta aca gag gac acg tcc acc ctg agt	1232
Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr Ser Thr Leu Ser	
345 350 355	
gat tct ctg agt gag aat ctg agc tta ttt ctg tgg tac ctg gtg cga	1280
Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp Tyr Leu Val Arg	
360 365 370	
ggc cta tgt ctc ttg ggg atc atg ctc tgg gga tca gtg tcc ctc acc	1328
Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser Val Ser Leu Thr	
375 380 385	
atg gtc acc ctg atc acc ctg cct ctg ctt ttc ctt ctg ccc aag aag	1376
Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu Leu Pro Lys Lys	
390 395 400	
gtg gga aaa tgg tac cag ttg ctg gaa gtg cag gtg cgg gaa tct ctg	1424
Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val Arg Glu Ser Leu	
405 410 415 420	
gca aag tcc agc cag gtg gcc att gag gct ctg tcg gcc atg cct aca	1472
Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser Ala Met Pro Thr	
425 430 435	
gtt cga agc ttt gcc aac gag gag ggc gaa gcc cag aag ttt agg gaa	1520
Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln Lys Phe Arg Glu	
440 445 450	
aag ctg caa gaa ata aag aca ctc aac cag aag gag gct gtg gcc tat	1568

Lys	Leu	Gln	Glu	Ile	Lys	Thr	Leu	Asn	Gln	Lys	Glu	Ala	Val	Ala	Tyr		
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Ala	Val	Asn	Ser	Trp	Thr	Thr	Ser	Ile	Ser	Gly	Met	Leu	Leu	Lys	Val		
	470						475				480						
gga	atc	ctc	tac	att	ggg	ggg	cag	ctg	gtg	acc	agt	ggg	gct	gta	agc	1664	
Gly	Ile	Leu	Tyr	Ile	Gly	Gly	Gln	Leu	Val	Thr	Ser	Gly	Ala	Val	Ser		
485					490					495					500		
agt	ggg	aac	ctt	gtc	aca	ttt	gtt	ctc	tac	cag	atg	cag	ttc	acc	cag	1712	
Ser	Gly	Asn	Leu	Val	Thr	Phe	Val	Leu	Tyr	Gln	Met	Gln	Phe	Thr	Gln		
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ggc	tcc	tca	gag	aaa	ata	ttt	gag	tac	ctg	gac	cgc	acc	cct	cgc	tgc	1808	
Gly	Ser	Ser	Glu	Lys	Ile	Phe	Glu	Tyr	Leu	Asp	Arg	Thr	Pro	Arg	Cys		
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Pro	Pro	Ser	Gly	Leu	Leu	Thr	Pro	Leu	His	Leu	Glu	Gly	Leu	Val	Gln		
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Phe	Gln	Asp	Val	Ser	Phe	Ala	Tyr	Pro	Asn	Arg	Pro	Asp	Val	Leu	Val		
565					570					575				580			
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gtg	gga	ccc	aat	ggg	tct	ggg	aag	agc	aca	gtg	gct	gcc	ctg	ctg	cag	2000	
Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Ala	Leu	Leu	Gln		
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aat	ctg	tac	cag	ccc	acc	ggg	gga	cag	ctg	ctg	ttg	gat	ggg	aag	ccc	2048	
Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	Gln	Leu	Leu	Leu	Asp	Gly	Lys	Pro		
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ctt	ccc	caa	tat	gag	cac	cgc	tac	ctg	cac	agg	cag	gtg	gct	gca	gtg	2096	

Leu Pro Gln Tyr Glu His Arg Tyr Leu His Arg Gln Val Ala Ala Val	
630 635 640	
gga caa gag cca cag gta ttt gga aga agt ctt caa gaa aat att gcc	2144
Gly Gln Glu Pro Gln Val Phe Gly Arg Ser Leu Gln Glu Asn Ile Ala	
645 650 655 660	
tat ggc ctg acc cag aag cca act atg gag gaa atc aca gct gct gca	2192
Tyr Gly Leu Thr Gln Lys Pro Thr Met Glu Glu Ile Thr Ala Ala Ala	
665 670 675	
gta aag tct ggg gcc cat agt ttc atc tct gga ctc cct cag ggc tat	2240
Val Lys Ser Gly Ala His Ser Phe Ile Ser Gly Leu Pro Gln Gly Tyr	
680 685 690	
gac aca gag gta gac gag gct ggg agc cag ctg tca ggg ggt cag cga	2288
Asp Thr Glu Val Asp Glu Ala Gly Ser Gln Leu Ser Gly Gly Gln Arg	
695 700 705	
cag gca gtg gcg ttg gcc cga gca ttg atc cgg aaa ccg tgt gta ctt	2336
Gln Ala Val Ala Leu Ala Arg Ala Leu Ile Arg Lys Pro Cys Val Leu	
710 715 720	
atc ctg gat gat gcc acc agt gcc ctg gat gca aac agc cag tta cag	2384
Ile Leu Asp Asp Ala Thr Ser Ala Leu Asp Ala Asn Ser Gln Leu Gln	
725 730 735 740	
gtg gag cag ctc ctg tac gaa agc cct gag cgg tac tcc cgc tca gtg	2432
Val Glu Gln Leu Leu Tyr Glu Ser Pro Glu Arg Tyr Ser Arg Ser Val	
745 750 755	
ctt ctc atc acc cag cac ctc agc ctg gtg gag cag gct gac cac atc	2480
Leu Leu Ile Thr Gln His Leu Ser Leu Val Glu Gln Ala Asp His Ile	
760 765 770	
ctc ttt ctg gaa gga ggc gct atc cgg gag ggg gga acc cac cag cag	2528
Leu Phe Leu Glu Gly Gly Ala Ile Arg Glu Gly Gly Thr His Gln Gln	
775 780 785	
ctc atg gag aaa aag ggg tgc tac tgg gcc atg gtg cag gct cct gca	2576
Leu Met Glu Lys Lys Gly Cys Tyr Trp Ala Met Val Gln Ala Pro Ala	
790 795 800	
gat gct cca gaa tgaaagcctt ctgagacctg cgcactccat ctccctccct	2628

Asp Ala Pro Glu

805

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tttcttctct ctgtggtgga gaaccacagc tgcagagtag gcagctgcct ccaggatgag 2688
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gctgatgctt tgggtgtggc agcactctga aactgagaaa tggtcagaat gtacggaaag 2868
atgatcagct attttcaaca taactgaagg catatgctgg ccataaaca ccctgtaggt 2928
tcttgatatt tataataaaa ttggtgtttt gt 2960

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<210> 48

<211> 808

<212> PRT

<213> Homo sapiens

<400> 48

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Leu Gly Gly Thr Arg Ser Phe Arg Pro His Arg Gly Ala Glu Ser Pro
          35          40          45

Arg Pro Gly Arg Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser
          50          55          60

Arg Cys Pro Ala Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu
65          70          75          80

Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu
          85          90          95

Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu
          100          105          110

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Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu
 115 120 125

Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser
 130 135 140

Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala
 145 150 155 160

Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu
 165 170 175

Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His
 180 185 190

Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu
 195 200 205

Pro Ala Ala Ala Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly
 210 215 220

Gly Gln Gly Gly Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu
 225 230 235 240

Gly Ser Glu Thr Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu
 245 250 255

Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr
 260 265 270

Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu
 275 280 285

Thr Leu Met Ser Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val
 290 295 300

Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val His Ser His Leu
 305 310 315 320

Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe
 325 330 335

Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr
 340 345 350

Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp
 355 360 365

Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser
 370 375 380

Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu
 385 390 395 400

Leu Pro Lys Lys Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val
 405 410 415

Arg Glu Ser Leu Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser
 420 425 430

Ala Met Pro Thr Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln
 435 440 445

Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu Asn Gln Lys Glu
 450 455 460

Ala Val Ala Tyr Ala Val Asn Ser Trp Thr Thr Ser Ile Ser Gly Met
 465 470 475 480

Leu Leu Lys Val Gly Ile Leu Tyr Ile Gly Gly Gln Leu Val Thr Ser
 485 490 495

Gly Ala Val Ser Ser Gly Asn Leu Val Thr Phe Val Leu Tyr Gln Met
 500 505 510

Gln Phe Thr Gln Ala Val Glu Val Leu Leu Ser Ile Tyr Pro Arg Val
 515 520 525

Gln Lys Ala Val Gly Ser Ser Glu Lys Ile Phe Glu Tyr Leu Asp Arg
 530 535 540

Thr Pro Arg Cys Pro Pro Ser Gly Leu Leu Thr Pro Leu His Leu Glu
 545 550 555 560

Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro
 565 570 575

Asp Val Leu Val Leu Gln Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu

580				585				590							
Val	Thr	Ala	Leu	Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala
		595					600					605			
Ala	Leu	Leu	Gln	Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	Gln	Leu	Leu	Leu
	610					615					620				
Asp	Gly	Lys	Pro	Leu	Pro	Gln	Tyr	Glu	His	Arg	Tyr	Leu	His	Arg	Gln
625					630					635					640
Val	Ala	Ala	Val	Gly	Gln	Glu	Pro	Gln	Val	Phe	Gly	Arg	Ser	Leu	Gln
				645					650					655	
Glu	Asn	Ile	Ala	Tyr	Gly	Leu	Thr	Gln	Lys	Pro	Thr	Met	Glu	Glu	Ile
			660					665					670		
Thr	Ala	Ala	Ala	Val	Lys	Ser	Gly	Ala	His	Ser	Phe	Ile	Ser	Gly	Leu
			675				680					685			
Pro	Gln	Gly	Tyr	Asp	Thr	Glu	Val	Asp	Glu	Ala	Gly	Ser	Gln	Leu	Ser
	690					695					700				
Gly	Gly	Gln	Arg	Gln	Ala	Val	Ala	Leu	Ala	Arg	Ala	Leu	Ile	Arg	Lys
705					710					715					720
Pro	Cys	Val	Leu	Ile	Leu	Asp	Asp	Ala	Thr	Ser	Ala	Leu	Asp	Ala	Asn
				725					730					735	
Ser	Gln	Leu	Gln	Val	Glu	Gln	Leu	Leu	Tyr	Glu	Ser	Pro	Glu	Arg	Tyr
			740					745					750		
Ser	Arg	Ser	Val	Leu	Leu	Ile	Thr	Gln	His	Leu	Ser	Leu	Val	Glu	Gln
		755					760					765			
Ala	Asp	His	Ile	Leu	Phe	Leu	Glu	Gly	Gly	Ala	Ile	Arg	Glu	Gly	Gly
	770					775					780				
Thr	His	Gln	Gln	Leu	Met	Glu	Lys	Lys	Gly	Cys	Tyr	Trp	Ala	Met	Val
785					790					795					800
Gln	Ala	Pro	Ala	Asp	Ala	Pro	Glu								
				805											

<210> 49
 <211> 3719
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97).. (2205)
 <223>

<400> 349
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 Met Arg Leu Pro Asp Leu
 1 5
 aga ccc tgg acc tcc ctg ctg ctg gtg gac gcg gct tta ctg tgg ctg 162
 Arg Pro Trp Thr Ser Leu Leu Leu Val Asp Ala Ala Leu Leu Trp Leu
 10 15 20
 ctt cag ggc cct ctg ggg act ttg ctt cct caa ggg ctg cca gga cta 210
 Leu Gln Gly Pro Leu Gly Thr Leu Leu Pro Gln Gly Leu Pro Gly Leu
 25 30 35
 tgg ctg gag ggg acc ctg cgg ctg gga ggg ctg tgg ggg ctg cta aag 258
 Trp Leu Glu Gly Thr Leu Arg Leu Gly Gly Leu Trp Gly Leu Leu Lys
 40 45 50
 cta aga ggg ctg ctg gga ttt gtg ggg aca ctg ctg ctc ccg ctc tgt 306
 Leu Arg Gly Leu Leu Gly Phe Val Gly Thr Leu Leu Leu Pro Leu Cys
 55 60 65 70
 ctg gcc acc ccc ctg act gtc tcc ctg aga gcc ctg gtc gcg ggg gcc 354
 Leu Ala Thr Pro Leu Thr Val Ser Leu Arg Ala Leu Val Ala Gly Ala
 75 80 85
 tca cgt gct ccc cca gcc aga gtc gct tca gcc cct tgg agc tgg ctg 402
 Ser Arg Ala Pro Pro Ala Arg Val Ala Ser Ala Pro Trp Ser Trp Leu
 90 95 100
 ctg gtg ggg tac ggg gct gcg ggg ctc agc tgg tca ctg tgg gct gtt 450
 Leu Val Gly Tyr Gly Ala Ala Gly Leu Ser Trp Ser Leu Trp Ala Val

105	110	115	
ctg agc cct cct gga gcc cag gag aag gag cag gac cag gtg aac aac			498
Leu Ser Pro Pro Gly Ala Gln Glu Lys Glu Gln Asp Gln Val Asn Asn			
120	125	130	
aaa gtc ttg atg tgg agg ctg ctg aag ctc tcc agg ccg gac ctg cct			546
Lys Val Leu Met Trp Arg Leu Leu Lys Leu Ser Arg Pro Asp Leu Pro			
135	140	145	150
ctc ctc gtt gcc gcc ttc ttc ttc ctt gtc ctt gct gtt ttg ggt gag			594
Leu Leu Val Ala Ala Phe Phe Phe Leu Val Leu Ala Val Leu Gly Glu			
	155	160	165
aca tta atc cct cac tat tct ggt cgt gtg att gac atc ctg gga ggt			642
Thr Leu Ile Pro His Tyr Ser Gly Arg Val Ile Asp Ile Leu Gly Gly			
	170	175	180
gat ttt gac ccc cat gcc ttt gcc agt gcc atc ttc ttc atg tgc ctc			690
Asp Phe Asp Pro His Ala Phe Ala Ser Ala Ile Phe Phe Met Cys Leu			
	185	190	195
ttc tcc ttt ggc agc tca ctg tct gca ggc tgc cga gga ggc tgc ttc			738
Phe Ser Phe Gly Ser Ser Leu Ser Ala Gly Cys Arg Gly Gly Cys Phe			
200	205	210	
acc tac acc atg tct cga atc aac ttg cgg atc cgg gag cag ctt ttc			786
Thr Tyr Thr Met Ser Arg Ile Asn Leu Arg Ile Arg Glu Gln Leu Phe			
215	220	225	230
tcc tcc ctg ctg cgc cag gac ctc ggt ttc ttc cag gag act aag aca			834
Ser Ser Leu Leu Arg Gln Asp Leu Gly Phe Phe Gln Glu Thr Lys Thr			
	235	240	245
ggg gag ctg aac tca cgg ctg agc tcg gat acc acc ctg atg agt aac			882
Gly Glu Leu Asn Ser Arg Leu Ser Ser Asp Thr Thr Leu Met Ser Asn			
	250	255	260
tgg ctt cct tta aat gcc aat gtg ctc ttg cga agc ctg gtg aaa gtg			930
Trp Leu Pro Leu Asn Ala Asn Val Leu Leu Arg Ser Leu Val Lys Val			
265	270	275	
gtg ggg ctg tat ggc ttc atg ctc agc ata tcg cct cga ctc acc ctc			978
Val Gly Leu Tyr Gly Phe Met Leu Ser Ile Ser Pro Arg Leu Thr Leu			

280	285	290	
ctt tct ctg ctg cac atg ccc ttc aca ata gca gcg gag aag gtg tac			1026
Leu Ser Leu Leu His Met Pro Phe Thr Ile Ala Ala Glu Lys Val Tyr			
295	300	305	310
aac acc cgc cat cag gaa gtg ctt cgg gag atc cag gat gca gtg gcc			1074
Asn Thr Arg His Gln Glu Val Leu Arg Glu Ile Gln Asp Ala Val Ala			
	315	320	325
agg gcg ggg cag gtg gtg cgg gaa gcc gtt gga ggg ctg cag acc gtt			1122
Arg Ala Gly Gln Val Val Arg Glu Ala Val Gly Gly Leu Gln Thr Val			
	330	335	340
cgc agt ttt ggg gcc gag gag cat gaa gtc tgt cgc tat aaa gag gcc			1170
Arg Ser Phe Gly Ala Glu Glu His Glu Val Cys Arg Tyr Lys Glu Ala			
	345	350	355
ctt gaa caa tgt cgg cag ctg tat tgg cgg aga gac ctg gaa cgc gcc			1218
Leu Glu Gln Cys Arg Gln Leu Tyr Trp Arg Arg Asp Leu Glu Arg Ala			
	360	365	370
ttg tac ctg ctc ata agg agg gtg ctg cac ttg ggg gtg cag atg ctg			1266
Leu Tyr Leu Leu Ile Arg Arg Val Leu His Leu Gly Val Gln Met Leu			
375	380	385	390
atg ctg agc tgt ggg ctg cag cag atg cag gat ggg gag ctc acc cag			1314
Met Leu Ser Cys Gly Leu Gln Gln Met Gln Asp Gly Glu Leu Thr Gln			
	395	400	405
ggc agc ctg ctt tcc ttt atg atc tac cag gag agc gtg ggg agc tat			1362
Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln Glu Ser Val Gly Ser Tyr			
	410	415	420
gtg cag acc ctg gta tac ata tat ggg gat atg ctc agc aac gtg gga			1410
Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp Met Leu Ser Asn Val Gly			
	425	430	435
gct gca gag aag gtt ttc tcc tac atg gac cga cag cca aat ctg cct			1458
Ala Ala Glu Lys Val Phe Ser Tyr Met Asp Arg Gln Pro Asn Leu Pro			
440	445	450	
tca cct ggc acg ctt gcc ccc acc act ctg cag ggg gtt gtg aaa ttc			1506
Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu Gln Gly Val Val Lys Phe			

455	460	465	470	
caa gac gtc tcc ttt gca tat ccc aat cgc cct gac agg cct gtg ctc				1554
Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro Asp Arg Pro Val Leu				
	475	480	485	
aag ggg ctg acg ttt acc cta cgt cct ggt gag gtg acg gcg ctg gtg				1602
Lys Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu Val Thr Ala Leu Val				
	490	495	500	
gga ccc aat ggg tct ggg aag agc aca gtg gct gcc ctg ctg cag aat				1650
Gly Pro Asn Gly Ser Gly Lys Ser Thr Val Ala Ala Leu Leu Gln Asn				
	505	510	515	
ctg tac cag ccc aca ggg gga cag gtg ctg ctg gat gaa aag ccc atc				1698
Leu Tyr Gln Pro Thr Gly Gly Gln Val Leu Leu Asp Glu Lys Pro Ile				
	520	525	530	
tca cag tat gaa cac tgc tac ctg cac agc cag gtg gtt tca gtt ggg				1746
Ser Gln Tyr Glu His Cys Tyr Leu His Ser Gln Val Val Ser Val Gly				
	535	540	545	550
cag gag cct gtg ctg ttc tcc ggt tct gtg agg aac aac att gct tat				1794
Gln Glu Pro Val Leu Phe Ser Gly Ser Val Arg Asn Asn Ile Ala Tyr				
	555	560	565	
ggg ctg cag agc tgc gaa gat gat aag gtg atg gcg gct gcc cag gct				1842
Gly Leu Gln Ser Cys Glu Asp Asp Lys Val Met Ala Ala Ala Gln Ala				
	570	575	580	
gcc cac gca gat gac ttc atc cag gaa atg gag cat gga ata tac aca				1890
Ala His Ala Asp Asp Phe Ile Gln Glu Met Glu His Gly Ile Tyr Thr				
	585	590	595	
gat gta ggg gag aag gga agc cag ctg gct gcg gga cag aaa caa cgt				1938
Asp Val Gly Glu Lys Gly Ser Gln Leu Ala Ala Gly Gln Lys Gln Arg				
	600	605	610	
ctg gcc att gcc cgg gcc ctt gta cga gac ccg cgg gtc ctc atc ctg				1986
Leu Ala Ile Ala Arg Ala Leu Val Arg Asp Pro Arg Val Leu Ile Leu				
	615	620	625	630
gat gag gct act agt gcc cta gat gtg cag tgc gag cag gcc ctg cag				2034
Asp Glu Ala Thr Ser Ala Leu Asp Val Gln Cys Glu Gln Ala Leu Gln				

635	640	645	
gac tgg aat tcc cgt ggg gat cgc aca gtg ctg gtg att gct cac agg			2082
Asp Trp Asn Ser Arg Gly Asp Arg Thr Val Leu Val Ile Ala His Arg			
650	655	660	
ctg cag gca gtt cag cgc gcc cac cag atc ctg gtg ctc cag gag ggc			2130
Leu Gln Ala Val Gln Arg Ala His Gln Ile Leu Val Leu Gln Glu Gly			
665	670	675	
aag ctg cag aag ctt gcc cag ctc cag gag gga cag gac ctc tat tcc			2178
Lys Leu Gln Lys Leu Ala Gln Leu Gln Glu Gly Gln Asp Leu Tyr Ser			
680	685	690	
cgc ctg gtt cag cag cgg ctg atg gac tgaggcccca gggatactgg			2225
Arg Leu Val Gln Gln Arg Leu Met Asp			
695	700		
gccctcttct caggggcgtc tccaggaccc agagctgttc ctgctttgag tttccctaga			2285
gctgtgcggc cagatagctg ttcctgagtt gcaagcacga tggagatttg gacactgtgt			2345
gcttttggtg ggggtggagag gtgggggtggg gtgggggtgtg gtgggggtggg aggctgtctg			2405
tgtccaggaa acttaattcc ctggtgacta gagctttgcc tggatgatgag gagtattttg			2465
tggcataata catatatattt aaaatatttt ctttcttacg tgaactgtat acattcatat			2525
agaaaattta gacaatataa aaaagtacaa agaagaaaag taaaagtacc cattgtttca			2585
cttcctggag ataaccatag ttgctatttt gctgcctgtc ccatcagtcg tttatctggt			2645
gtttgagata gaaattaacc aaaaatgaca taaatattca tgagattgcc ttcctatata			2705
cttccttggt cctaccagtg tctgctattt tgaagaagct agggctctgga gggacagaga			2765
acagttccct gattaacagt attaatagcg acattggtaa cagctaccat ttatagagtt			2825
ttaatgggag taggagctat gctaagtgtt tttcatgtat tatcgttttt aatcattatc			2885
cccaacccta tgaggtttgt tattatcccc attttacaga tgaggaaact gaagctcaaa			2945
gaggetcaat gactttccca aggtggtcgt agtggtggag ttggagtttg aacacaggcc			3005

tgaccctaga gtccacaccc tgaccaatc aattatattg catcttgggt ccataaaccc 3065
 taatccataa tcccatcaag aaaagctctg ctgctcttag ctctaaataa ttcagaatct 3125
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 caccagagag gtttctctac cattagcttc cctcttccgg ccattcttca caaagtcatt 3245
 tttctaaatt ctgtgtcaca tacgatgatg gcatttctgg aaattccttc aggtgctctc 3305
 aagccctgct gcagagatcc ttttcagagc acacactgtt ccagcccatc tgtctcaccc 3365
 tctcctgttg tatccagctc cagcaciaac tttctgcctt cccaacacc tttgtgcctt 3425
 tgcatatggg gttttcttgc ccattttctg ctgactcgc ccctgatttt caagttcaag 3485
 acttaactca ggggttcaggt ctccaggag gccttactta tgtcgtcagt ctggggaact 3545
 ctccatgtgc ttctatcact gtgcgggttac ctctttcaca gcccttttaa agttctatct 3605
 tccctttccc accttttttg accttccact agaccatgag cacctgggcg gaaagccata 3665
 tatcttatta agctttatat ctgctacctg gccgagggt aattcatagt ggag 3719

<210> 50
 <211> 703
 <212> PRT
 <213> Homo sapiens

<400> 50

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Ala	Ala	Leu	Leu	Trp	Leu	Leu	Gln	Gly	Pro	Leu	Gly	Thr	Leu	Leu	Pro
			20					25					30		
Gln	Gly	Leu	Pro	Gly	Leu	Trp	Leu	Glu	Gly	Thr	Leu	Arg	Leu	Gly	Gly
			35				40					45			
Leu	Trp	Gly	Leu	Leu	Lys	Leu	Arg	Gly	Leu	Leu	Gly	Phe	Val	Gly	Thr
			50				55					60			

Leu Leu Leu Pro Leu Cys Leu Ala Thr Pro Leu Thr Val Ser Leu Arg
 65 70 75 80

Ala Leu Val Ala Gly Ala Ser Arg Ala Pro Pro Ala Arg Val Ala Ser
 85 90 95

Ala Pro Trp Ser Trp Leu Leu Val Gly Tyr Gly Ala Ala Gly Leu Ser
 100 105 110

Trp Ser Leu Trp Ala Val Leu Ser Pro Pro Gly Ala Gln Glu Lys Glu
 115 120 125

Gln Asp Gln Val Asn Asn Lys Val Leu Met Trp Arg Leu Leu Lys Leu
 130 135 140

Ser Arg Pro Asp Leu Pro Leu Leu Val Ala Ala Phe Phe Phe Leu Val
 145 150 155 160

Leu Ala Val Leu Gly Glu Thr Leu Ile Pro His Tyr Ser Gly Arg Val
 165 170 175

Ile Asp Ile Leu Gly Gly Asp Phe Asp Pro His Ala Phe Ala Ser Ala
 180 185 190

Ile Phe Phe Met Cys Leu Phe Ser Phe Gly Ser Ser Leu Ser Ala Gly
 195 200 205

Cys Arg Gly Gly Cys Phe Thr Tyr Thr Met Ser Arg Ile Asn Leu Arg
 210 215 220

Ile Arg Glu Gln Leu Phe Ser Ser Leu Leu Arg Gln Asp Leu Gly Phe
 225 230 235 240

Phe Gln Glu Thr Lys Thr Gly Glu Leu Asn Ser Arg Leu Ser Ser Asp
 245 250 255

Thr Thr Leu Met Ser Asn Trp Leu Pro Leu Asn Ala Asn Val Leu Leu
 260 265 270

Arg Ser Leu Val Lys Val Val Gly Leu Tyr Gly Phe Met Leu Ser Ile
 275 280 285

Ser Pro Arg Leu Thr Leu Leu Ser Leu Leu His Met Pro Phe Thr Ile
 290 295 300

Ala Ala Glu Lys Val Tyr Asn Thr Arg His Gln Glu Val Leu Arg Glu
305 310 315 320

Ile Gln Asp Ala Val Ala Arg Ala Gly Gln Val Val Arg Glu Ala Val
325 330 335

Gly Gly Leu Gln Thr Val Arg Ser Phe Gly Ala Glu Glu His Glu Val
340 345 350

Cys Arg Tyr Lys Glu Ala Leu Glu Gln Cys Arg Gln Leu Tyr Trp Arg
355 360 365

Arg Asp Leu Glu Arg Ala Leu Tyr Leu Leu Ile Arg Arg Val Leu His
370 375 380

Leu Gly Val Gln Met Leu Met Leu Ser Cys Gly Leu Gln Gln Met Gln
385 390 395 400

Asp Gly Glu Leu Thr Gln Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln
405 410 415

Glu Ser Val Gly Ser Tyr Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp
420 425 430

Met Leu Ser Asn Val Gly Ala Ala Glu Lys Val Phe Ser Tyr Met Asp
435 440 445

Arg Gln Pro Asn Leu Pro Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu
450 455 460

Gln Gly Val Val Lys Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg
465 470 475 480

Pro Asp Arg Pro Val Leu Lys Gly Leu Thr Phe Thr Leu Arg Pro Gly
485 490 495

Glu Val Thr Ala Leu Val Gly Pro Asn Gly Ser Gly Lys Ser Thr Val
500 505 510

Ala Ala Leu Leu Gln Asn Leu Tyr Gln Pro Thr Gly Gly Gln Val Leu
515 520 525

Leu Asp Glu Lys Pro Ile Ser Gln Tyr Glu His Cys Tyr Leu His Ser

530		535		540
Gln Val Val Ser Val Gly Gln Glu Pro Val Leu Phe Ser Gly Ser Val				
545		550		555
				560
Arg Asn Asn Ile Ala Tyr Gly Leu Gln Ser Cys Glu Asp Asp Lys Val				
	565		570	575
Met Ala Ala Ala Gln Ala Ala His Ala Asp Asp Phe Ile Gln Glu Met				
	580		585	590
Glu His Gly Ile Tyr Thr Asp Val Gly Glu Lys Gly Ser Gln Leu Ala				
	595		600	605
Ala Gly Gln Lys Gln Arg Leu Ala Ile Ala Arg Ala Leu Val Arg Asp				
	610		615	620
Pro Arg Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Val Gln				
	625		630	635
				640
Cys Glu Gln Ala Leu Gln Asp Trp Asn Ser Arg Gly Asp Arg Thr Val				
	645		650	655
Leu Val Ile Ala His Arg Leu Gln Ala Val Gln Arg Ala His Gln Ile				
	660		665	670
Leu Val Leu Gln Glu Gly Lys Leu Gln Lys Leu Ala Gln Leu Gln Glu				
	675		680	685
Gly Gln Asp Leu Tyr Ser Arg Leu Val Gln Gln Arg Leu Met Asp				
	690		695	700

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 <212> DNA
 <213> human herpesvirus 1

<220>
 <221> CDS
 <222> (1).. (264)
 <223>

<400> 51

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gtt ggg ccc agg acg tac gcc gac gta cgc gat gag atc aat aaa agg 96
 Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg
 20 25 30

ggg cgt gag gac cgg gag gcg gcc aga acc gcc gtg cac gac ccg gag 144
 Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu
 35 40 45

cgt ccc ctg ctg cgc tct ccc ggg ctg ctg ccc gaa atc gcc ccc aac 192
 Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn
 50 55 60

gca tcc ttg ggt gtg gca cat cga aga acc ggc ggg acc gtg acc gac 240
 Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp
 65 70 75 80

agt ccc cgt aat ccg gta acc cgt 264
 Ser Pro Arg Asn Pro Val Thr Arg
 85

<210> 52

<211> 88

<212> PRT

<213> human herpesvirus 1

<400> 52

Met Ser Trp Ala Leu Glu Met Ala Asp Thr Phe Leu Asp Thr Met Arg
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Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg
 20 25 30

Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu
 35 40 45

Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn
 50 55 60

Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp
65 70 75 80

Ser Pro Arg Asn Pro Val Thr Arg
85

<210> 53
<211> 549
<212> DNA
<213> Human cytomegalovirus

<220>
<221> CDS
<222> (1).. (549)
<223>

<400> 53
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Met Asp Leu Leu Ile Arg Leu Gly Phe Leu Leu Met Cys Ala Leu Pro
1 5 10 15
acc ccc ggt gag cgg tct tcg cgt gac ccg aaa acc ctt ctc tct ctg 96
Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu
20 25 30
tct ccg cga caa caa gct tgt gtt ccg aga acg aag tcg cac aga ccc 144
Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro
35 40 45
gtt tgt tac aac gat aca ggg gac tgc aca gat gca gat gat agc tgg 192
Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp
50 55 60
aaa cag ctg ggt gag gac ttt gcg cac caa tgc ttg cag gcg gcg aaa 240
Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys
65 70 75 80
aag agg cct aaa acg cac aaa tcc cgt ccg aac gat agg aac ctt gag 288
Lys Arg Pro Lys Thr His Lys Ser Arg Pro Asn Asp Arg Asn Leu Glu
85 90 95
ggg agg ctg acc tgt caa cga gtc cgt cgg cta ctg ccc tgt gat ttg 336
Gly Arg Leu Thr Cys Gln Arg Val Arg Arg Leu Leu Pro Cys Asp Leu

100	105	110	
gat att cat cct agc cac cgg ttg tta acg ctt atg aat aac tgc gtc			384
Asp Ile His Pro Ser His Arg Leu Leu Thr Leu Met Asn Asn Cys Val			
115	120	125	
tgt gac ggg gcc gtt tgg aac gcg ttt cgc ttg ata gaa cga cac gga			432
Cys Asp Gly Ala Val Trp Asn Ala Phe Arg Leu Ile Glu Arg His Gly			
130	135	140	
ttc ttc gct gtg act ttg tat tta tgt tgc ggg att act ctg ctg gtt			480
Phe Phe Ala Val Thr Leu Tyr Leu Cys Cys Gly Ile Thr Leu Leu Val			
145	150	155	160
gtt att cta gca ttg ctg tgc agc ata aca tac gaa tcg act gga cgt			528
Val Ile Leu Ala Leu Leu Cys Ser Ile Thr Tyr Glu Ser Thr Gly Arg			
165	170	175	
ggg att cga cgt tgt ggc tcc			549
Gly Ile Arg Arg Cys Gly Ser			
180			

<210> 54
 <211> 183
 <212> PRT
 <213> Human cytomegalovirus

<400> 54

Met Asp Leu Leu Ile Arg Leu Gly Phe Leu Leu Met Cys Ala Leu Pro			
1	5	10	15
Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu			
20	25	30	
Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro			
35	40	45	
Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp			
50	55	60	
Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys			
65	70	75	80

Lys	Arg	Pro	Lys	Thr	His	Lys	Ser	Arg	Pro	Asn	Asp	Arg	Asn	Leu	Glu	85	90	95	
Gly	Arg	Leu	Thr	Cys	Gln	Arg	Val	Arg	Arg	Leu	Leu	Pro	Cys	Asp	Leu	100	105	110	
Asp	Ile	His	Pro	Ser	His	Arg	Leu	Leu	Thr	Leu	Met	Asn	Asn	Cys	Val	115	120	125	
Cys	Asp	Gly	Ala	Val	Trp	Asn	Ala	Phe	Arg	Leu	Ile	Glu	Arg	His	Gly	130	135	140	
Phe	Phe	Ala	Val	Thr	Leu	Tyr	Leu	Cys	Cys	Gly	Ile	Thr	Leu	Leu	Val	145	150	155	160
Val	Ile	Leu	Ala	Leu	Leu	Cys	Ser	Ile	Thr	Tyr	Glu	Ser	Thr	Gly	Arg	165	170	175	
Gly	Ile	Arg	Arg	Cys	Gly	Ser										180			